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600-1-266

FIGURE 1A

SEQ ID NO:1

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1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc
121 ggcgaaagga agcggttgag gcgcttgaa cccgaaaagt ctcggtgctc ctggctacct
181 cgcacagcgg tgcccgcccg gccgtcagta ccatggacag cagcgctgcc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgctact caagttgctc cccagcaccg agccccgggt
301 cctgggtcaa cttgtcccac ttagatggca acctgtccga cccatgcggg ccgaaccgca
361 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cagtccctcc atgatcacgg
421 ccatacagat catggccctc tactccatcg tgtgcgtggg ggggctcttc ggaaacttcc
481 tggatcatgta tgtgattgtc agatacacca agatgaagac tggcaccac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtaccct gcccttccag agtgtgaatt
601 acctaattgg aacatggcca ttgggaacca tcttttgaa gatagtgat tccatagatt
661 actataacat gttcaccagc atattcacc tctgcaccat gagtgttgat cgatacattg
721 cagtctgcca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaa ctggatcctc tcttcagcca ttggtcttcc tgtaatgttc atggctacaa
841 caaaatacag gcaagggtcc atagattgta cactaacatt ctctcatcca acctgggtact
901 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgctcatca
961 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcatg ctctctggct
1021 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctggtg gtgggtggctg
1081 tgttcacgtg ctgctggact cccattcaca ttacgtcat cattaaaggc ttgggtacaa
1141 tcccagaaac tacgttccag actgtttctt ggcacttctg cattgctcta ggttacacaa
1201 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca
1261 gagagtctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1321 agaacactag agaccacccc tccacggcca atacagtga tagaactaat catcagctag
1381 aaaatctgga agcagaaact gctccgttgc cctaacaggg tctcatgcca ttcgacctt
1441 caccaagctt agaagccacc atgtatgtgg aagcagggtg cttcaagaat gtgtaggagg
1501 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca
1561 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttggg aggaaaggaa
1621 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaacaaa acccatcgtg
1681 gtatgtgaat tgaagtcac ataaaagggtg accttctgt ctgtaagatt ttattttcaa
1741 gcaaatatct atgacctcaa caaagaagaa ccatcttttg ttaagttcac cgtagtaaca
1801 cataaagtaa atgctacctc tgatcaaagc acctgaaatg gaagggtccg gtctttttag
1861 tgtttttgca agggaatgaa tccattatct tatttttagac ttttaacttc aacttaaaat
1921 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1981 aataacatct ctttcatcta gctccataat tgcaaggga gagattagca tgaaaggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaaatactt
2101 ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtgggttg ttcctggaat
2161 tc

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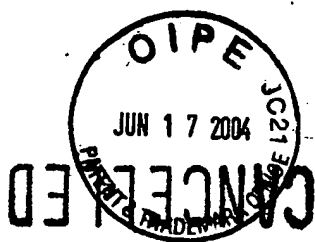


600-1-266.

FIGURE 1B

SEQ ID NO:2

Met	Asp	Ser	Ser	Ala	Ala	Pro	Thr	Asn	Ala	Ser	Asn	Cys	Thr	Asp	Ala
1				5					10					15	
Leu	Ala	Tyr	Ser	Ser	Cys	Ser	Pro	Ala	Pro	Ser	Pro	Gly	Ser	Trp	Val
			20					25					30		
Asn	Leu	Ser	His	Leu	Asp	Gly	Asn	Leu	Ser	Asp	Pro	Cys	Gly	Pro	Asn
		35					40					45			
Arg	Thr	Asn	Leu	Gly	Gly	Arg	Asp	Ser	Leu	Cys	Pro	Pro	Thr	Gly	Ser
	50					55					60				
Pro	Ser	Met	Ile	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val
	65				70					75					80
Cys	Val	Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val
				85					90					95	
Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu
			100					105					110		
Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val
		115					120					125			
Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile
	130					135					140				
Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu
	145				150					155					160
Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys
				165					170					175	
Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys
			180					185					190		
Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Met	Ala
	195						200					205			
Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser
	210					215					220				
His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Val	Lys	Ile	Cys	Val	Phe	Ile
	225				230					235					240
Phe	Ala	Phe	Ile	Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu
				245					250					255	
Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu
			260					265				270			
Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val
		275					280					285			
Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Tyr	Val	Ile	Ile
	290					295					300				
Lys	Ala	Leu	Val	Thr	Ile	Pro	Glu	Thr	Thr	Phe	Gln	Thr	Val	Ser	Trp
	305				310					315					320
His	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr	Asn	Ser	Cys	Leu	Asn	Pro	Val
				325					330					335	
Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe	Lys	Arg	Cys	Phe	Arg	Glu	Phe
			340					345					350		
Cys	Ile	Pro	Thr	Ser	Ser	Asn	Ile	Glu	Gln	Gln	Asn	Ser	Thr	Arg	Ile
		355					360					365			
Arg	Gln	Asn	Thr	Arg	Asp	His	Pro	Ser	Thr	Ala	Asn	Thr	Val	Asp	Arg
	370					375					380				
Thr	Asn	His	Gln	Leu	Glu	Asn	Leu	Glu	Ala	Glu	Thr	Ala	Pro	Leu	Pro
	385					390				395					400



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FIGURE 2A

SEQ ID NO:3

```
1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc
121 ggcgaaaagga agcggctgag gcgcttgga cccgaaaagt ctcggtgctc ctggctacct
181 cgcacagcgg tgcccggccc gccgtcagta ccatggacag cagcgtgcc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgctact caagttggcc cccagcacc agccccgggt
301 cctgggtcaa cttgtcccac ttagatggca acctgtccga cccatgcggt ccgaaccgca
361 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cagtcctctc atgatcacgg
421 ccatcacgat catggccctc tactccatcg tgtgcgtggt ggggctcttc ggaaacttcc
481 tggctcatgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtaccct gcccttcag agtgtgaatt
601 acctaatggg aacatggcca tttggaacca tcctttgcaa gatagtgat tccatagatt
661 actataacat gttcaccagc atattcacc tctgcaccat gagtgttgat cgatacattg
721 cagtctgcca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaa ctggatcctc tcttcagcca ttggtcttcc tgtaatgttc atggctacaa
841 caaaatacac gcaagggtcc atagattgta cactaacatt ctctcatcca acctggtact
901 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgtcatca
961 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcag ctctctggct
1021 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctgggt gtggtggctg
1081 tgttcatcgt ctgctggact cccattcaca tttacgtcat cattaaagcc ttggttacaa
1141 tcccagaaac tacgttccag actgtttctt ggcacttctg cattgctcta ggttacacaa
1201 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgaatgttca
1261 gagagtcttg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1321 agaactctag agaccacccc tccacggcca atacagtga tagaactaat catcagctag
1381 aaaatctgga agcagaaact gctccgttgc cctaacaggg tctcatgcca tccgacctt
1441 caccaagctt agaagccacc atgtatgtgg aagcaggttg cttcaagaat gtgtaggagg
1501 ctctaattct ctaggaaaagt gcctactttt aggtcatcca acctctttcc tctctggcca
1561 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttggg aggaaaggaa
1621 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaacaaa acccatcgtg
1681 gtatgtgaat tgaagtcac ataaaagggt acccttctgt ctgtaagatt ttattttcaa
1741 gcaaatattt atgacctcaa caaagaagaa ccattctttg ttaagttcac cgtagtaaca
1801 cataaagtaa atgctacctc tgatcaaagc accttgaatg gaaggtecca gtctttttag
1861 tgtttttgca agggaaatgaa tccattatc tatttttagac ttttaacttc aacttaaaat
1921 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1981 aataacatct ctttcatcta gctccataat tgcaaggga gagattagca tgaaaggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaaatactt
2101 ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtgggttg ttcctggaat
2161 tc
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600-1-266 FIGURE 2B

SEQ ID NO:4

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15
Leu Ala Tyr Ser Ser Cys Pro Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30
Asn Leu Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn
35 40 45
Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
50 55 60
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
65 70 75 80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
85 90 95
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
100 105 110
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
115 120 125
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
130 135 140
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
145 150 155 160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
165 170 175
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
180 185 190
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
195 200 205
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
210 215 220
His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
225 230 235 240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
245 250 255
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
260 265 270
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
275 280 285
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
290 295 300
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
305 310 315 320
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
325 330 335
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
340 345 350
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
355 360 365
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
370 375 380
Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
385 390 395 400



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FIGURE 3A

SEQ ID NO:5

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc
121 ggcgaaagga agcggctgag gcgcttgga cccgaaaagt ctcggtgctc ctggctacct
181 cgcacagcgg tgcccgcgg gccgtcagta ccatggacag cagcgtgccc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgctact caagttgctc cccagcaccc agccccgggt
301 cctgggtcaa cttgtccac ttagatggca acctgaccga cccatgcggt ccgaaccgca
361 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cagtccctcc atgatcacgg
421 ccatcacgat catggccctc tactccatcg tgtgcgtggg ggggctcttc ggaaacttcc
481 tggatcatgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtaccct gcccttccag agtgtgaatt
601 acctaatggg aacatggcca tttggaacca tcctttgcaa gatagtgc tccatagatt
661 actataacat gttcaccagc atattcaccc tctgcacccat gagtgttgat cgatacattg
721 cagtctgcca cctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaa ctggatcctc tcttcagcca ttggctcttc tgtaatgttc atggctacaa
841 caaaatacag gcaagggttcc atagattgta cactaacatt ctctcatcca acctgggtact
901 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgctcatca
961 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcatg ctctctgggt
1021 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctgggt gtgggtggctg
1081 tgttcatcgt ctgctggact cccattcaca ttacgtcat cattaaagcc ttggttacaa
1141 tcccagaaac tacgttccag actgtttctt ggcacttctg cattgctcta ggttacacaa
1201 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca
1261 gagagtcttg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1321 agaagactag agaccacccc tccacggcca atacagtga tagaactaat catcagctag
1381 aaaatctgga agcagaaact gctccgttgc cctaacaggg tctcatgcca ttccgacctt
1441 caccaagctt agaagccacc atgtatgtgg aagcaggttg cttcaagaat gtgtaggagg
1501 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctcttccc tctctggcca
1561 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttggg aggaaaggaa
1621 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaacaaa acccatcgtg
1681 gtatgtgaat tgaagtcac ataaaagggt acccttctgt ctgtaagatt ttattttcaa
1741 gcaaatattt atgacctcaa caaagaagaa ccatcttttg ttaagttcac cgtagtaaca
1801 cataaagtaa atgctacctc tgatcaaagc accttgaatg gaagggtccga gtcttttttag
1861 tgtttttgca agggaaatgaa tccattatcc tatttttagac ttttaacttc aacttaaaat
1921 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1981 aataacatct ctttcatcta gctccataat tgcaagggaa gagattagca tgaagggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaaatactt
2101 ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtgggttg ttcttggaa
2161 tc



600-1-266' FIGURE 3B

SEQ ID NO:6

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30
Asn Leu Ser His Leu Asp Gly Asn Leu Thr Asp Pro Cys Gly Pro Asn
35 40 45
Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
50 55 60
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
65 70 75 80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
85 90 95
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
100 105 110
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
115 120 125
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
130 135 140
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
145 150 155 160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
165 170 175
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
180 185 190
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
195 200 205
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
210 215 220
His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
225 230 235 240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
245 250 255
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
260 265 270
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
275 280 285
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
290 295 300
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
305 310 315 320
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
325 330 335
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
340 345 350
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
355 360 365
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
370 375 380
Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
385 390 395 400



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FIGURE 4

SEQ ID NO:7

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcage
121 ggcgaaagga agcggctgag gcgcttgaa cccgaaaagt ctcggtgctc ctggctacct
181 cgcacagcgg tgcccgcgg gccgtcagta ccatggacag cagcgctgcc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgtagt caagtgtgct cccagcaccc agccccgggt
301 cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgcggg ccgaaccgca
361 ccaatctggg cgggagagac agcctgtgcc ctccgaccgg cagtcctctc atgatcacgg
421 ccatacagat catggccctc tactccatcg tgtgcgtggg ggggctcttc ggaaacttcc
481 tggatcatgta tgtgattgtc agatacaca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtaccct gcccttcag agtgtgaatt
601 acctaattggg aacatggcca tttggaacca tcctttgcaa gatagtatc tccatagatt
661 actataacat gttcaccagc atattcacc tctgcaccat gagtgtgat cgatacattg
721 cagtctgcca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaa ctggatctc tcttcagcca ttggtcttcc tgtaatgttc atggctacaa
841 caaaatacag gcaagggtcc atagattgta cactaacatt ctctcatcca acctggtact
901 gggaaaacct cgtgaagatc tgtgttttca tcttcgctt cattatgcca gtgctcatca
961 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcatg ctctctgggt
1021 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctgggt gtggtgggtg
1081 tgttcatcgt ctgctggact cccattcaca ttacgtcat cattaaaggc ttggttacaa
1141 tcccagaaac tacgttccag actgtttctt ggcacttctg cattgtctta ggttacacaa
1201 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgaatgttca
1261 gagagtctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1321 agaaccactag agaccacccc tccacggcca atacagtga tagaactaat catcagctag
1381 aaaatctgga agcagaaact gctccgttgc cctaacaggg tctcatgcca ttcggacctt
1441 caccaagctt agaagccacc atgtatgtgg aagcaggtt cttcaagaat gtgtaggagg
1501 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctcttcc tctctggcca
1561 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttgga aggaaaggaa
1621 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaacaaa acccatcgtg
1681 gtatgtgaat tgaagtcac ataaaagggtg acccttctgt ctgtaagatt ttattttcaa
1741 gcaaatatct atgacctcaa caaagaagaa ccatcttttg ttaagttcac cgtagtaaca
1801 cataaagtaa atgtacctc tgatcaaagc acctggaatg gaaggtecca gtctttttag
1861 tgtttttgca agggaatgaa tccattatc tatttttagac ttttaacttc aacttaaaat
1921 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1981 aataacatct ctttcatcta gctccataat tgcaaggga gagattagca tgaaaggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aagggtgatt ctcatgcact ncaaatactt
2101 ccaaagagtc atcatggggg atttttcatt cttaggctt cagtgggttg ttcttggaa
2161 tc



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FIGURE 5

SEQ ID NO:8

```
1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcgggtccc ctccgectga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc
121 ggcgaaaagga agcggctgag gcgcttgaa cccgaaaagt ctcggtgctc ctggctacct
181 cgcacagcgg tgcccggccg gccgtcagta ccattggacag cagcgctgcc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgctact caagttgctc cccagcaccg agccccgggt
301 cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgcggg ccgaaccgca
361 ccaacctggg cgggagagac agcctatgcc ctccgaccgg cagtcctctc atgatcacgg
421 ccacacgat catggccctc tactccatcg tgtgcgtggg ggggctcttc ggaaacttcc
481 tggcatgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtacctt gcccttccag agtgtgaatt
601 acctaatggg aacatggcca ttggaaacca tcttttgcaa gatagtgatc tccatagatt
661 actataacat gttcaccagc atattcacc tctgcaccat gagtgttgat cgatacattg
721 cagtctgcca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaa ctggatcctc tcttcagcca ttggctcttc tgtaatgttc atggctacaa
841 caaaatacag gcaagggttc atagattgta cactaacatt ctctcatcca acctgggtact
901 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgctcatca
961 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcagc ctctctggct
1021 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctggtg gtggtggctg
1081 tgttcatcgt ctgctggact cccattcaca ttacgtcat cattaaagcc ttggttacaa
1141 tcccagaaac tacgttccag actgtttctt ggcacttctg cattgctcta ggttacacaa
1201 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca
1261 gagagttctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1321 agaacactag agaccacccc tccacggcca atacagtga tagaactaat catcagctag
1381 aaaatctgga agcagaaact gctccgttgc cctaacaggg tctcatgcca tccgacctt
1441 caccaagctt agaagccacc atgtatgtgg aagcagggtg cttcaagaat gtgtaggagg
1501 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctcttccc tctctggcca
1561 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttggg aggaaaggaa
1621 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaccaa acccatcgtg
1681 gtatgtgaat tgaagtcac ataaaagggtg acccttctgt ctgtaagatt ttattttcaa
1741 gcaaatattt atgacctcaa caaagaagaa ccatcttttg ttaagttcac cgtagtaaca
1801 cataaagtaa atgctacctc tgatcaaagc accttgaatg gaagggtccg gtctttttag
1861 tgtttttgca agggaatgaa tccattattc tatttttagac ttttaacttc aacttaaaat
1921 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1981 aataacatct ctttcatcta gctccataat tgcaaggga gagattagca tgaaaggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aagggttgatt ctcatgcact ncaaatactt
2101 ccaaagagtc atcatggggg atttttcatt cttaggcttt cagtgggttg ttcttggaaat
2161 tc
```



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FIGURE 6A

SEQ ID NO:9

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gtcgggtccc ctccgctga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaagaa acagcaggag ctgtggcagc
121 ggcgaaagga agcggctgag gcgcttgga cccgaaaagt ctcggtgctc ctgggtacct
181 cgcacagcgg tgcccggccc gccgtcagta ccatggacag cagcgctgcc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgact caagttgctc cccagcacc agccccgggt
301 cctgggtcaa cttgtccac ttataggcca acctgtccga cccatgctgt ccgaaccgca
361 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cgccagtcctcc atgatcacgg
424 ccatcacgat catggccctc tactccatcg tgtgcgtggg ggggctcttc ggaaacttcc
484 tggatcatgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
544 tcaaccttgc tctggcagat gccttagcca ccagtacct gcccttccag agtgtgaatt
604 acctaatggg aacatggcca tttggaacca tctttgcaa gatagtgat tccatagatt
664 actataacat gttcaccagc atattcacc tctgcacat gagtggtgat cgatacattg
724 cagtctgcca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
784 atgtctgcaa ctggatcctc tcttcagcca ttggtcttcc tgtaatgttc atgggtacaa
844 caaataacag gcaaggttcc atagattgta cactaacatt ctctcatcca acctgggtact
904 gggaaaacct cgtgaagatc tgtgttttca tcttcgcctt cattatgcca gtgtcatca
964 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgtccgcatg ctctctgggt
1024 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgtgggtg gtgggtgggtg
1084 tgttcatcgt ctgctggact ccatttcaca ttacgtcat cattaaagcc ttggttacaa
1144 tcccagaaac tacgttccag actgtttctt ggcacttctg cattgtctca ggttacacaa
1204 acagctgcct caaccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca
1264 gagagttctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1324 agaactctgga agaccacccc tccacggcca atacagtgga tagaactaat catcagctag
1384 aaaatctgga agcagaaact gtcctgttgc cctaacaggg tctcatgcca ttcgacctt
1444 caccaagctt agaagccacc atgtatgtgg aagcagggtg cttcaagaat gtgtaggagg
1504 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca
1564 ctctgctctg cacattagag ggacagccaa aagtaagtgg agcatttggg aggaaaggaa
1624 tataccacac cgaggagtcc agtttgtgca agacaccag tggaaccaa acccatcgtg
1684 gtatgtgaat tgaagtcac ataaaagggt acccttctgt ctgtaagatt ttattttcaa
1744 gcaaatattt atgacctcaa caaagaagaa ccatcttttg ttaagttcac cgtagtaaca
1804 cataaagtaa atgctacctc tgatcaaagc accttgaatg gaagggtccga gtctttttag
1864 tgtttttgca agggaatgaa tccattatc tatttttagac ttttaacttc aacttaaaat
1924 tagcatctgg ctaaggcatc attttcacct ccatttcttg gttttgtatt gtttaaaaaa
1984 aataacatct ctttcatcta gtcacataat tgcaaggga gagattagca tgaaaggtaa
2044 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaataactt
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2164 tc

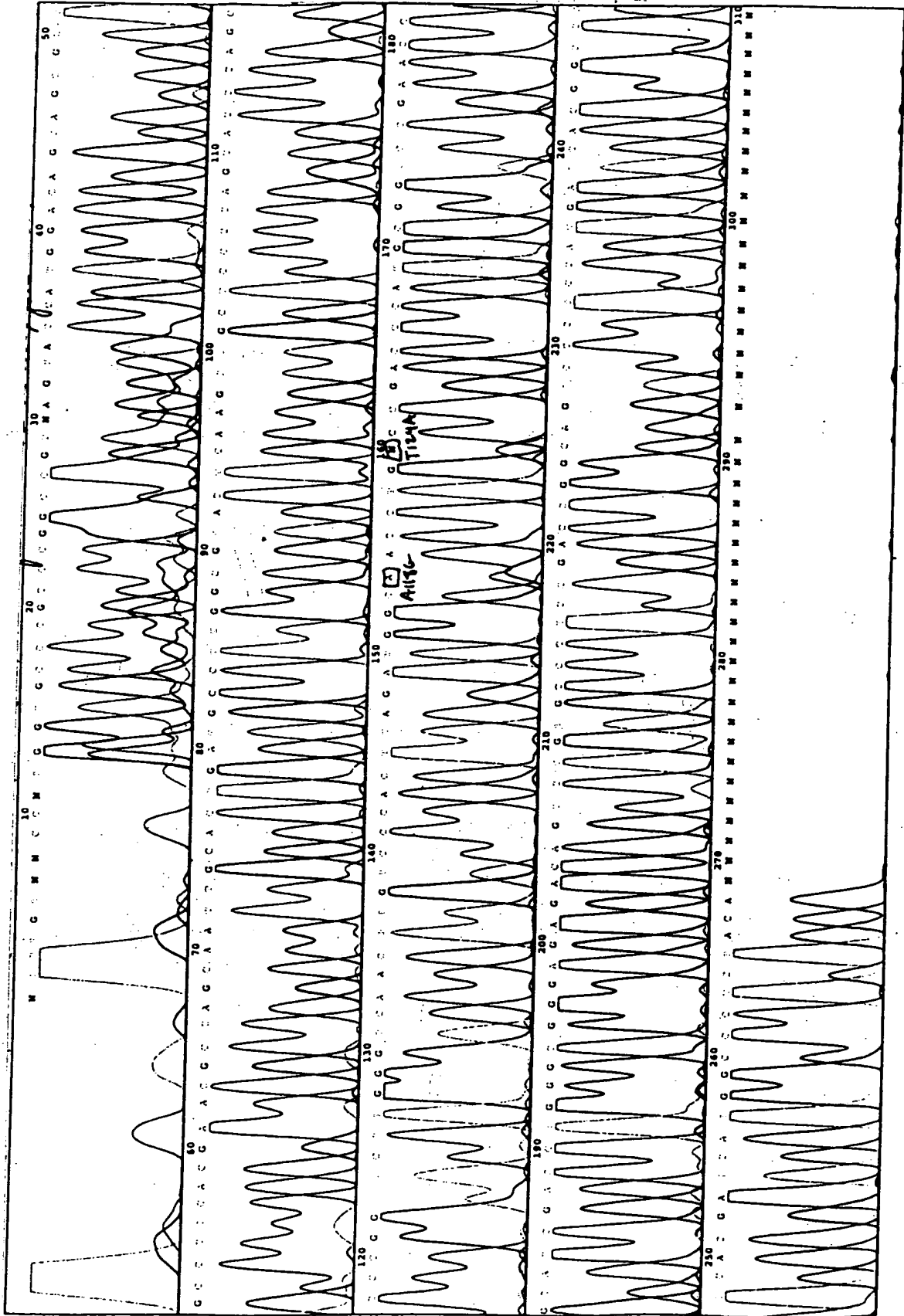
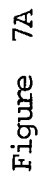


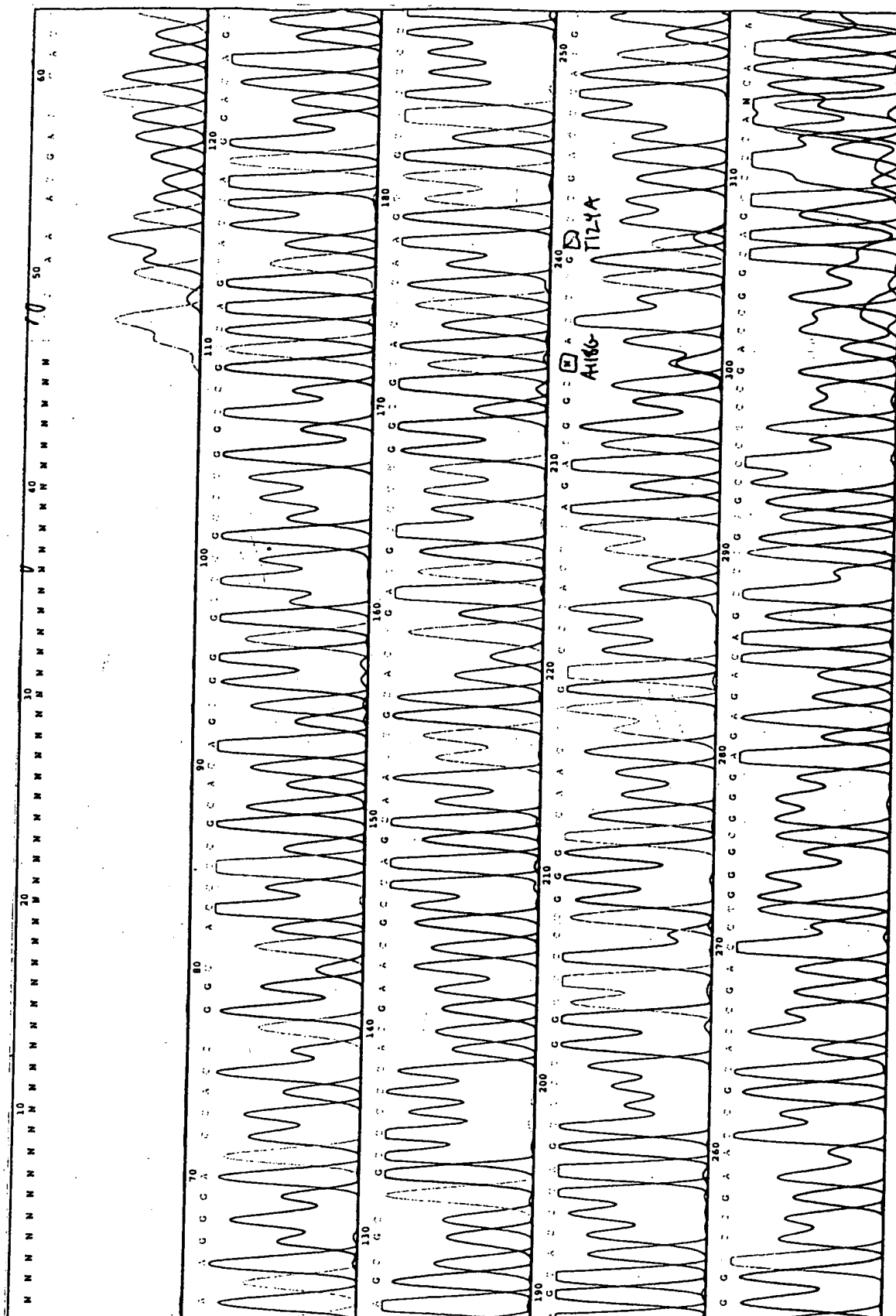
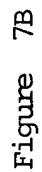
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FIGURE 6B

SEQ ID NO:10

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30
Asn Leu Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn
35 40 45
Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Gly Ser
50 55 60
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
66 71 76 81
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
86 91 96
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
101 106 111
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
116 121 126
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
131 136 141
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
146 151 156 161
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
166 171 176
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
181 186 191
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
196 201 206
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
211 216 221
His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
226 231 236 241
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
246 251 256
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
261 266 271
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
276 281 286
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
291 296 301
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
306 311 316 321
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
326 331 336
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
341 346 351
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
356 361 366
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
371 376 381
Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
386 391 396 401





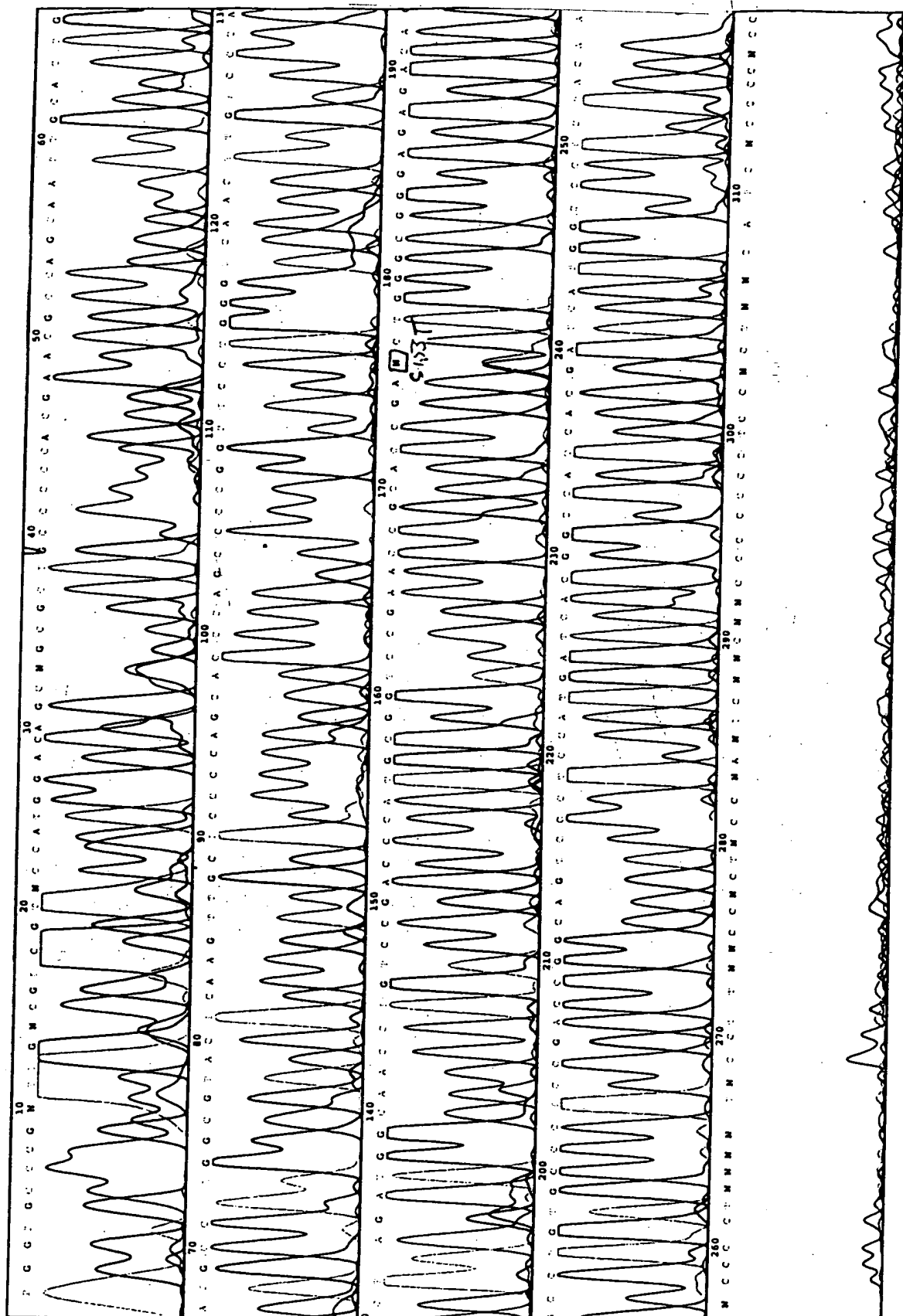
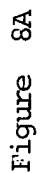


Figure 8B

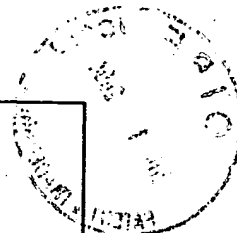
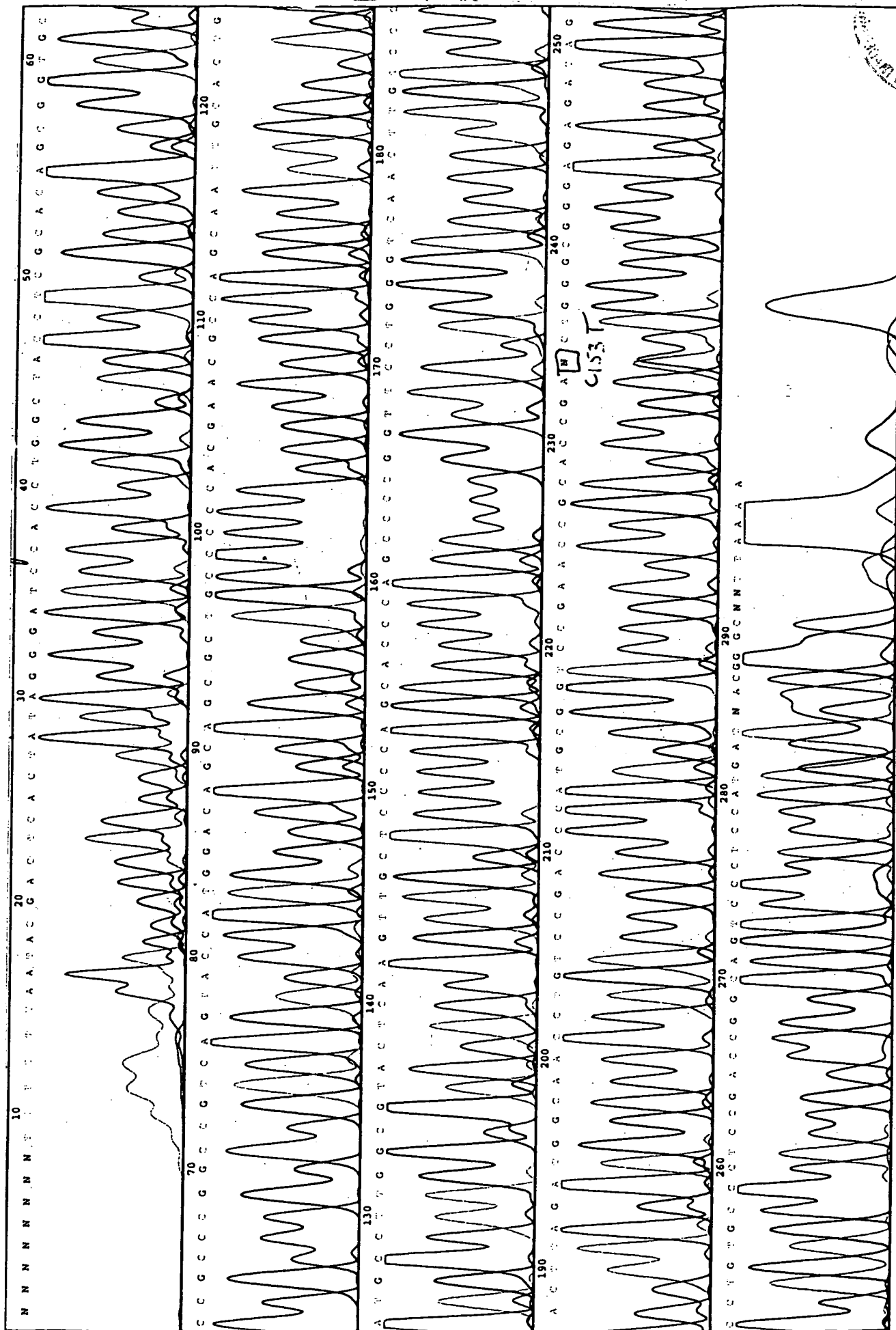
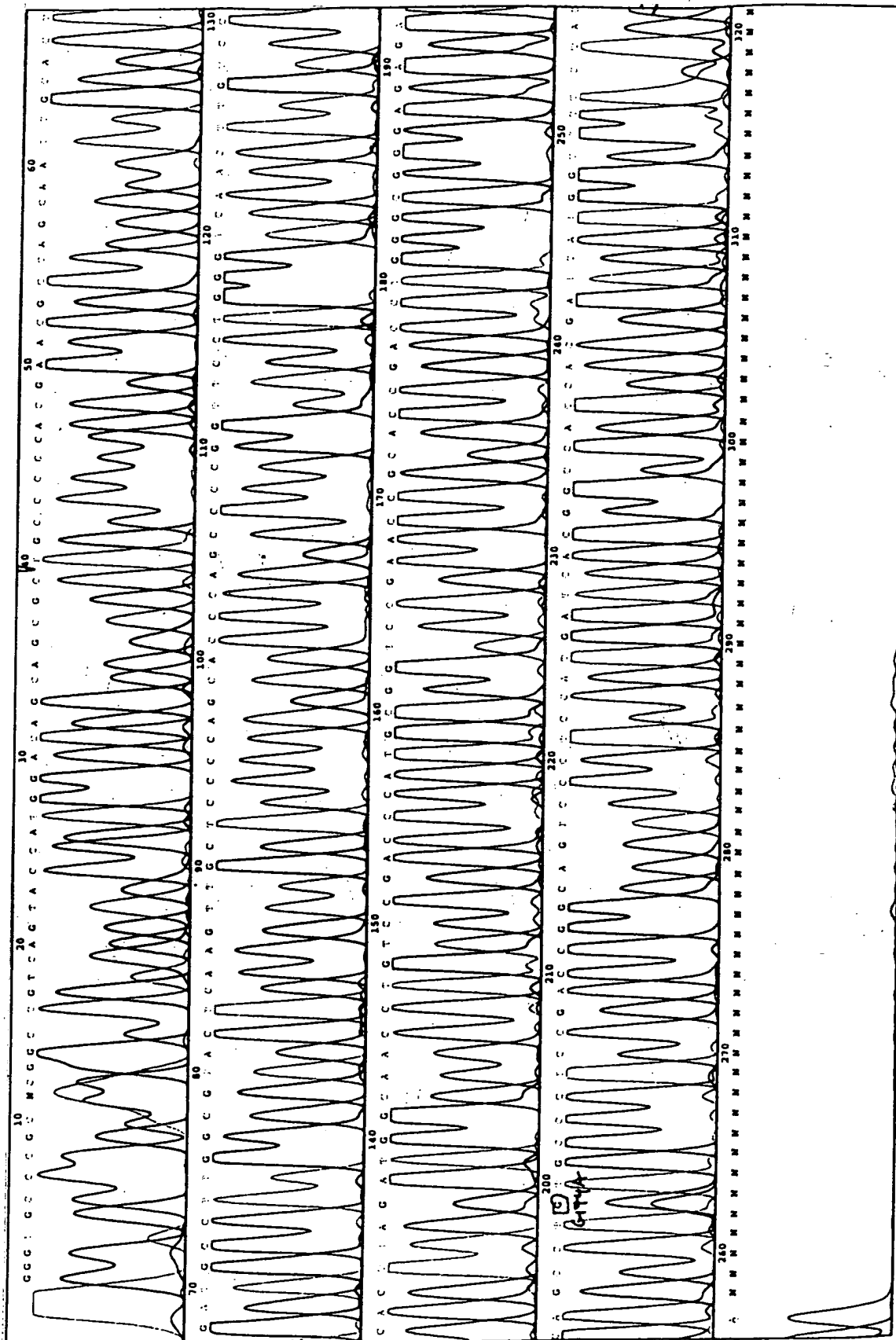
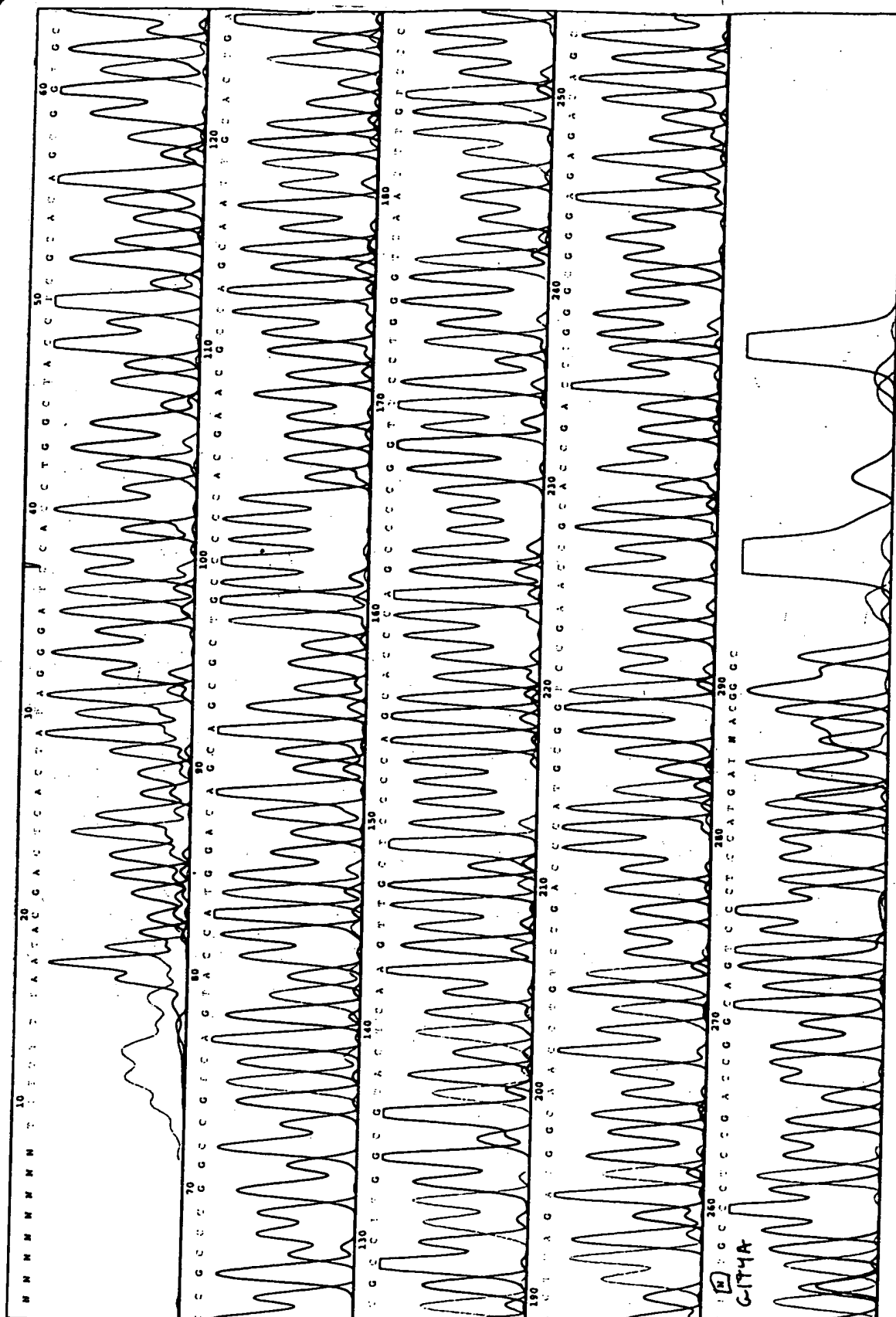
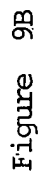
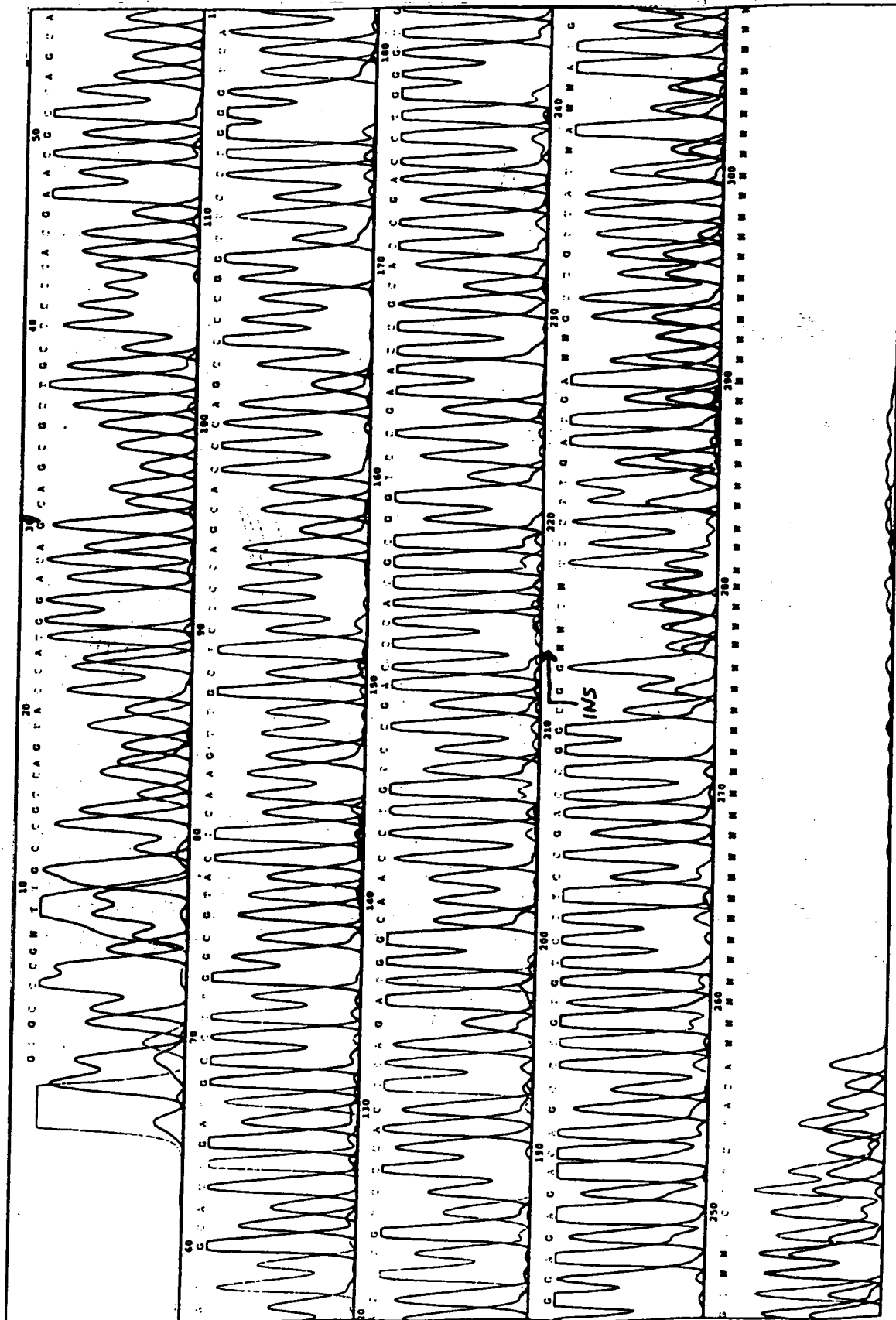
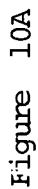


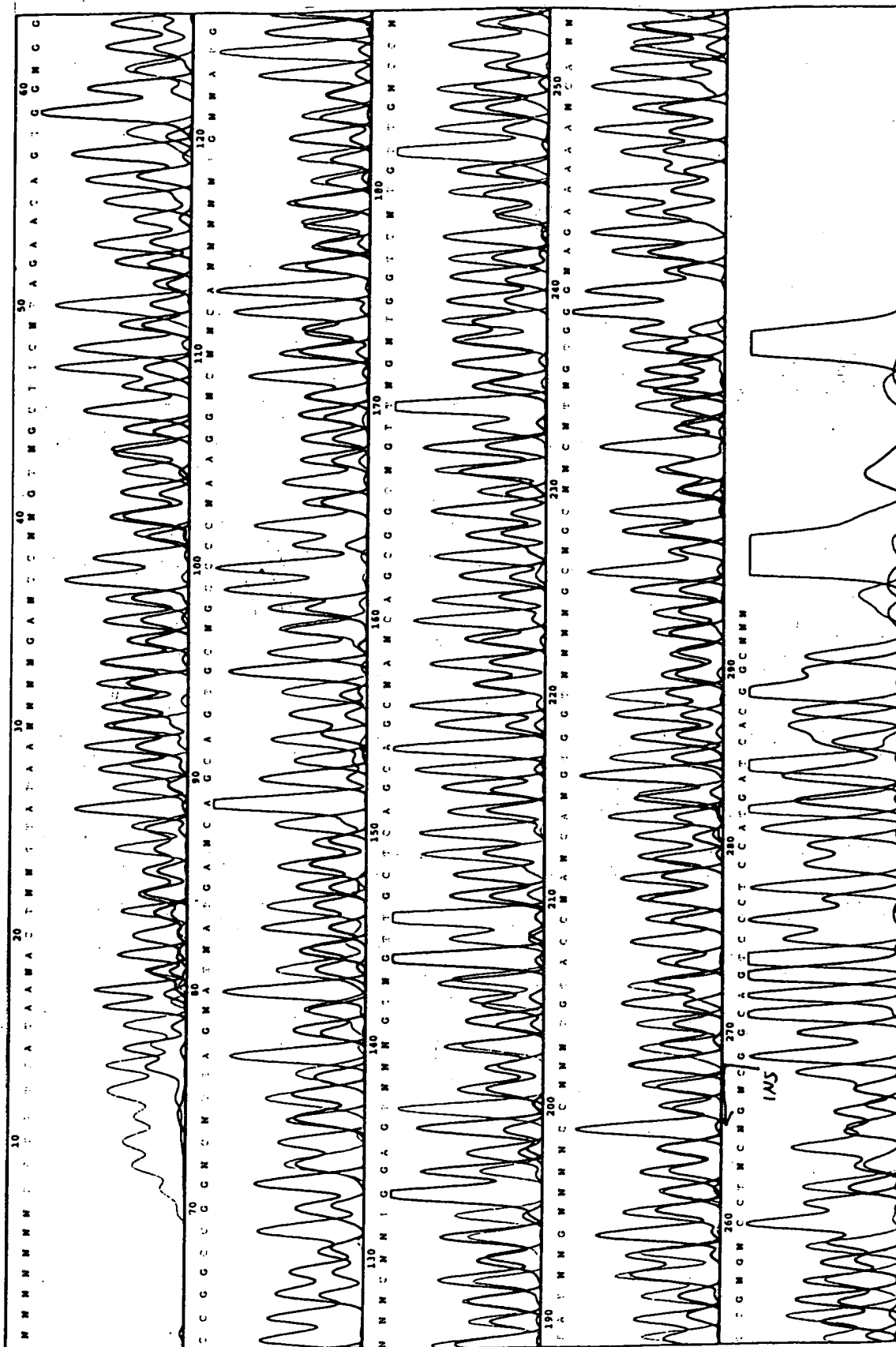
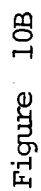


Figure 9A









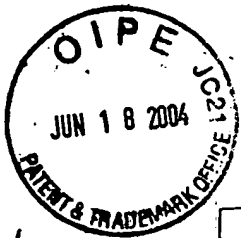


Figure 11A

